

-1-

SEQUENCE LISTING

<110> National Institute of Allergy and Infectious Diseases, NIH
 Transkaryotic Therapies, Inc.
 Garman, Scott C.
 Garboczi, David N.
 Selden, Richard F.
 Treco, Douglas A.
 Kinoshita, Carol M.
 Borowski, Marianne

<120> CRYSTAL STRUCTURE OF HUMAN ALPHA-GALACTOSIDASE

<130> 0502WO

<150> US 60/536,451
 <151> 2004-01-13

<160> 2

<170> PatentIn version 3.2

<210> 1
 <211> 1290
 <212> DNA
 <213> Homo sapiens

<400> 1
 atgcagctga ggaaccaga actacatctg ggctgcgcgc ttgcgcttcg cttcctggcc 60
 ctcgtttctt gggacatccc tggggctaga gcaactggaca atggattggc aaggacgcct 120
 accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180
 gattcctgca tcagtggaaa gctcttcatg gagatggcag agctcatggt ctcagaaggc 240
 tggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaga 300
 gattcagaag gcagacttca ggcagaccct cagcgctttc ctcattggat tcgccagcta 360
 gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa 420
 acctgcgcag gcttccctgg gagttttgga tactacgaca ttgatgcca gacctttgct 480
 gactggggag tagatctgct aaaatttgat ggttggtact gtgacagttt ggaaaatttg 540
 gcagatgggt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600
 tctgtgagt ggctcttta tatgtggccc ttcaaaagc ccaattatac agaaatccga 660
 cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720
 agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780
 ggttggaatg acccagatat gttagtgatt ggcaactttg gcctcagctg gaatcagcaa 840
 gtaactcaga tggccctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc 900
 cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat 960
 caggaccctt tgggcaagca aggttaccag cttagacagg gagacaactt tgaagtgtgg 1020
 gaacgacctc tctcaggctt agcctgggct gtagctatga taaaccggca ggagattggg 1080
 ggacctcgct cttataccat cgcagttgct tccctgggta aaggagtggc ctgtaatcct 1140
 gcctgcttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaatggact 1200
 tcaaggttaa gaagtcacat aaatcccaca ggcactgttt tgcttcagct agaaaatata 1260
 atgcagatgt cattaaaaga cttactttta 1290

<210> 2
 <211> 429
 <212> PRT
 <213> Homo sapiens

-2-

<400> 2

```

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
1      5      10      15
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
20      25      30
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
35      40      45
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
50      55      60
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
65      70      75      80
Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
85      90      95
Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
100     105     110
Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
115     120     125
Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
130     135     140
Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
145     150     155     160
Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
165     170     175
Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
180     185     190
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
195     200     205
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
210     215     220
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
225     230     235     240
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
245     250     255
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
260     265     270
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
275     280     285
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
290     295     300

```

-3-

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
 305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
 325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
 370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
 405 410 415

Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu
 420 425